

Exhibit 4

1 of 2

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:37:29 / Search time 91.4866 Seconds  
(without alignments)  
291.060 Million cell updates/sec

Title: 09782816-51  
Perfect score: 251  
Sequence: 1 GVKETPQKXQRLHVEQEL.....BSATEBKLPVLAQKLAAL 52

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251	100.0	400	1	DCT2_HUMAN
2	248	98.8	401	1	DCT2_MOUSE
3	248	98.8	402	1	Q6A7H5
4	220	87.6	403	2	Q61RB3
5	213	84.9	403	2	Q66J30
6	211	84.1	338	2	Q7ZXY2
7	177	70.5	402	2	Q9PRG6
8	177	70.5	405	2	Q7T3H1
9	76	30.3	402	2	Q61P53
10	72.5	28.9	380	2	Q9VAY9
11	71	28.3	800	2	Q6MVP7
12	71	28.3	813	2	Q7SH14
13	70	27.9	311	2	Q971V5
14	70	27.9	751	2	Q8WQX1
15	70	27.9	1087	2	Q86B55
16	70	27.9	1124	2	Q8M0J8
17	70	27.9	2199	2	Q7PUP2
18	69.5	27.7	873	2	Q95X56
19	69.5	27.7	919	2	Q95X55
20	68	27.1	1755	2	Q7RV31
21	68	27.1	1868	2	Q8X0C5
22	67.5	26.9	1868	2	Q6BNV2
23	67	26.7	455	2	Q7ZVF1
24	67	26.7	639	2	Q62245
25	67	26.7	1795	2	Q91CJ9
26	67	26.7	2478	2	Q91CH2
27	67	26.7	2478	2	Q91L69
28	67	26.7	2481	2	Q99QR6
29	67	26.7	2481	2	Q7A4B1
30	66	26.3	393	2	Q49567
31	66	26.3	860	2	Q7Q0Q9

32	66	26.3	866	2	Q84500	084500 chlamydia t
33	66	26.3	1022	2	Q8TBY8	08TBY8 homo sapien
34	65.5	26.1	1837	2	Q74424	074424 schizosacch
35	65	25.9	388	2	Q7P225	07P225 anopheles g
36	64.5	25.7	348	2	Q8L1J9	08L1J9 cryza sativ
37	64	25.5	149	2	Q9B2S3	09B2S3 homo sapien
38	64	25.5	188	2	Q9UM00	09UM00 homo sapien
39	64	25.5	188	2	Q921L3	0921L3 mus musculu
40	64	25.5	188	2	Q6DGM9	06DGM9 brachydanto
41	64	25.5	210	2	Q9S1Y3	09S1Y3 arabidopsis
42	64	25.5	230	2	Q75545	075545 homo sapien
43	64	25.5	1227	1	J1P3_DROME	099GFI drosophila
44	64	25.5	1956	2	Q9Y2K3	09Y2K3 homo sapien
45	63.5	25.3	163	1	Y012_BHPI	P51714 bacterioph

ALIGNMENTS

RESULT 1  
DCT2\_HUMAN STANDARD; PRT; 400 AA.  
AC Q13561; Q86YN2; Q9BM17;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)  
DB (p50 dynamitin) (DCTN-50) (Dyactin 2).  
GN Name=DCTN2; Synonyms=DCTN50;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=96178072; PubMed=8647893; DOI=10.1083/jcb.132.4.617;  
RA Echeverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.;  
RT "Molecular characterization of the 50-kD subunit of dynactin reveals  
RT organization during mitosis."  
RT J. Cell Biol. 132:617-633(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta, Skin, and Uterus;  
RX MEDLINE=2238257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh P.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Panje C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,  
RA Boes S.A., McKernan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywicki M.T., Skalska U., Smalins D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE OF 1-384 FROM N.A.  
RA Amats U.P., Yu-Lee L.-Y.;  
RT "Human 50 kD dynactin subunit, p50 dynamitin, isolated from HeLa  
RT cells."  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-13.

2052  
Eclibit 4

RC TISSUE-Platelet; PubMed=12665801; DOI=10.1038/nbr1810;  
 RA MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbr1810;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Maris A., Rubin G.M., Hong L.,  
 RA Stapanian M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rabe S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC [2]  
 RN SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320,  
 RP SUBCELLULAR LOCATION: AND DEVELOPMENTAL STAGE.  
 RC TISSUE=Brain;  
 RA MEDLINE=97289622; PubMed=9144527; DOI=10.1006/dbrc.1997.6447;  
 RA Abe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.;  
 RT "The presence of the 50-kDa subunit of dynein complex in the nerve  
 RT growth cone.";  
 RL Biochem. Biophys. Res. Commun. 233:295-299 (1997).  
 CC [3]  
 RN INTERACTION WITH BICD2.  
 RP MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;  
 RA Hoogenraad C.C., Akmanova A., Howell S.A., Dottiand B.R.,  
 RA de Zeeuw C.I., Willemsen R., Visser F., Grosveld F., Galjart N.;  
 RT "Mammalian Goli-1-associated Bicaudal-D2 functions in the dynein-  
 RT dynein pathway by interacting with these complexes.";  
 RL EMBO J. 20:4041-4054 (2001).  
 CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,  
 CC and plays a role in prometaphase chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development.  
 CC -1- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U50733; AAC50423.1; -;  
 CC EMBL; BC000718; AAH00718.1; -;  
 CC EMBL; BC000946; AAH09468.1; -;  
 CC EMBL; BC014083; AAH14083.1; -;  
 CC EMBL; AY189155; AAO34395.1; -;  
 CC Genew; HGNC:2712; DCTN2.  
 CC MIM; 607376; -;  
 CC DR GO; GO:0005813; C:centrosome; TAS.  
 CC DR GO; GO:0005869; C:dynein complex; TAS.  
 CC DR GO; GO:0000776; C:kinechochore; TAS.  
 CC DR GO; GO:0008283; P:cell proliferation; TAS.  
 CC DR GO; GO:0007067; P:mitosis; TAS.  
 CC DR InterPro; IPR006996; Dynein.  
 CC DR Pfam; PF04912; Dynein; 1.  
 CC DR KX Colled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 CC Membrane; Microtubule; Motor protein.  
 CC FT INIT MET 0  
 CC FT DOMAIN 98 131 Coiled coil (Potential).  
 CC FT DOMAIN 213 243 Coiled coil (Potential).  
 CC FT DOMAIN 378 398 Coiled coil (Potential).  
 CC FT CONFLICT 34 34 A -> AFAQEL (in Ref. 1).  
 CC FT CONFLICT 35 35 B -> ELR (in Ref. 3).  
 CC FT CONFLICT 381 384 LATV -> PGHS (in Ref. 3).  
 CC SEQUENCE 400 AA; 44099 MW; 0A55AB55C0BB270F CRC64;  
 CC  
 CC Query Match 100.0%; Score 251; DB 1; Length 400;  
 CC Best Local Similarity 100.0%; Pred. No. 4.7e-17;  
 CC Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 GYKHPQKQKQRLHVEQLTTEVEKIKTYKESATREKLTPLAKQAL 52  
 CC 93 GYKHPQKQKQRLHVEQLTTEVEKIKTYKESATREKLTPLAKQAL 144  
 CC  
 CC RESULT 2  
 CC DCT2\_MOUSE STANDARD; PRT; 401 AA.  
 CC AC Q99KJ8;  
 CC DR 28-FEB-2003 (Rel. 41, Created)  
 CC DR 05-JUL-2004 (Rel. 44, Last sequence update)  
 CC DR 05-JUL-2004 (Rel. 44, Last annotation update)  
 CC DR Dynein complex 50 kDa subunit (50 kDa dynein-associated polypeptide)  
 CC DR (p50 dynein) (DCTN-50) (Dynein 2) (Growth cone membrane protein  
 CC DR 23-48k) (GMP23-48k).  
 CC DR Name=Dctn2;  
 CC DR Mus musculus (Mouse).  
 CC DR Bakayocia; Mezzacasa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC DR Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC DR NCBI TaxID=10090;

RP SEQUENCE FROM N.A.  
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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 RA de Zeeuw C.I., Willemsen R., Visser F., Grosveld F., Galjart N.;  
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 CC and plays a role in prometaphase chromosome alignment and spindle  
 CC organization during mitosis. May play a role in synapse formation  
 CC during brain development.  
 CC -1- SUBUNIT: Subunit of dynein, a multiprotein complex associated  
 CC with dynein (By similarity). Interacts with BICD2.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC -1- DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic  
 CC and membrane-associated forms in neonates. Levels of membrane-  
 CC associated form are greatly reduced in the adult.  
 CC CC  
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 CC  
 CC EMBL; BC004613; AAH04613.1; -;  
 CC WGD; WGI:107733; Dctn2.  
 CC DR InterPro; IPR006996; Dynein.  
 CC DR Pfam; PF04912; Dynein; 1.  
 CC DR Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 CC DR Membrane; Microtubule; Motor protein.  
 CC FT INIT MET 0  
 CC FT DOMAIN 98 131 By similarity.  
 CC FT DOMAIN 214 244 Coiled coil (Potential).  
 CC SEQUENCE 401 AA; 43985 MW; 1535E4ABD5940EBC CRC64;  
 CC  
 CC Query Match 98.8%; Score 248; DB 1; Length 401;  
 CC Best Local Similarity 98.1%; Pred. No. 9.4e-17;  
 CC Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;